We claim:

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1. A process for production of compounds of the general formula I

$$\begin{array}{c|c}
CH_2 & CH_2 \\
\hline
CH=CH & CH_2 \\
\hline
CH_2 & CH_3
\end{array}$$
(I)

in transgenic organisms with a content of at least 1% by weight of these compounds based on the total lipid content of the transgenic organism, which comprises the following process steps:

- a) introducing, into the organism, at least one nucleic acid sequence which encodes an ω -3-desaturase activity, and
- b) culturing the organism under conditions which permits the production of
 compounds of the general formula I, and

where the variables and substituents in formula I have the following meanings:

R¹ = hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lyso-diphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the formula II

$$H_{2}C-O-R^{2}$$
 $HC-O-R^{3}$
 $H_{2}C-O$
(II),

- R^2 = hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated C_2 - C_{24} -alkylcarbonyl,
- R^3 = hydrogen, saturated or unsaturated C_2 - C_{24} -alkylcarbonyl, or R^2 and R^3 independently of one another are a radical of the formula la:

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$$\begin{array}{c|c} O & CH_2 \\ \hline \\ CH = CH \end{array} \begin{array}{c} CH_2 \\ \hline \\ CH_2 \\ \hline \end{array} \begin{array}{c} CH_3 \\ \hline \end{array} \begin{array}$$

n = 2, 3, 4, 5, 6, 7 or 9, m = 2, 3, 4, 5 or 6 and p = 0 or 3.

- 2. The process according to claim 1, wherein in addition to the nucleic acid sequence introduced in item a), which codes for an ω -3-desaturase activity, further nucleic acid sequences which code for polypeptides with Δ 9-elongase, Δ 6-desaturase, Δ 8-desaturase, Δ 6-elongase, Δ 5-desaturase, Δ 5-elongase or Δ 4-desaturase activity are introduced.
- 3. The process according to claim 1 or 2, wherein the substituents R² or R³ independently of one another are saturated or unsaturated C₁₈-C₂₂-alkylcarbonyl.
 - 4. The process according to claims 1 to 3, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18} -, C_{20} or C_{22} -alkylcarbonyl with at least two double bonds.
- 5. The process according to claims 1 to 4, wherein the transgenic organism is a transgenic microorganism or a transgenic plant.
 - 6. The process according to claims 1 to 5, wherein the transgenic organism is an oil-producing plant, a vegetable plant or an ornamental.
- The process according to claims 1 to 6, wherein the transgenic organism is a transgenic plant selected from the group of the plant families Adelotheciaceae,
 Anacardiaceae, Asteraceae, Apiaceae, Betulaceae, Boraginaceae,
 Brassicaceae, Bromeliaceae, Caricaceae, Cannabaceae, Convolvulaceae,
 Chenopodiaceae, Crypthecodiniaceae, Cucurbitaceae, Ditrichaceae,
 Elaeagnaceae, Ericaceae, Euphorbiaceae, Fabaceae, Geraniaceae,
 Gramineae, Juglandaceae, Lauraceae, Leguminosae, Linaceae or
 Prasinophyceae.
 - 8. The process according to claims 1 to 7, wherein the compounds of the general formula I are isolated from the organism in the form of their oils, lipids or free fatty acids.

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- 9. The process according to claims 1 to 8, wherein the compounds of the general formula I are isolated in a concentration of at least 5% by weight based on the total lipid content of the transgenic organism.
- 10. An oil, lipid or fatty acid or a fraction thereof, produced by the process accordingto any of claims 1 to 9.
 - 11. An oil, lipid or fatty acid composition which comprises PUFAs produced by a process according to any of claims 1 to 9 and which originates from transgenic plants.
- A process for the production of oils, lipids or fatty acid compositions by mixing
 oil, lipids or fatty acids according to claim 10 or an oil, lipid or fatty acid
 composition according to claim 11 with oils, lipids or fatty acids of animal origin.
 - 13. The use of oil, lipids or fatty acids according to claim 10, oil, lipid or fatty acid composition according to claim 11 or oils, lipids or fatty acid compositions produced according to claim 12 in feed, foodstuffs, cosmetics or pharmaceuticals.
 - 14. An isolated nucleic acid sequence which codes for polypeptides with ω -3-desaturase activity, selected from the group consisting of:
 - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
 - nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 2, or
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 2 and which have ω -3-desaturase activity.
- 25 15. The isolated nucleic acid sequence according to claim 14, wherein the sequence is derived from an alga, a fungus, a microorganism or a nonhuman animal.
 - 16. The isolated nucleic acid sequence according to claim 14 or 15, wherein the sequence is derived from the family Pythiaceae.

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- 17. An amino acid sequence which is encoded by an isolated nucleic acid sequence according to any of claims 14 to 16.
- 18. A gene construct comprising an isolated nucleic acid according to any of claims14 to 16, wherein the nucleic acid is linked functionally to one or more regulatory signals.
- The gene construct according to claim 18, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s).
- The gene construct according to claim 18 or 19, wherein the nucleic acid construct additionally comprises biosynthesis genes of the fatty acid or lipid metabolism selected from the group Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ8-desaturase, Δ9-desaturase, Δ12-desaturase, Δ6-elongase, Δ5-elongase or Δ9-elongase.
- 20 21. A vector comprising a nucleic acid according to claims 14 to 16 or a gene construct according to claim 18.
 - 22. A transgenic nonhuman organism comprising at least one nucleic acid according to claims 14 to 16, a gene construct according to claim 18 or a vector according to claim 21.
- 25 23. The transgenic nonhuman organism according to claim 22, wherein the organism is a microorganism, a nonhuman animal or a plant.
 - 24. The transgenic nonhuman organism according to claim 22 or 23, wherein the organism is a plant.